

AMENDMENTS TO THE CLAIMS

Listing of claims:

1. (Previously presented) A method for identifying herbicides comprising utilizing a 2-methyl-6-solanylbenzoquinone methyltransferase.
2. (Previously presented) The method according to claim 1, wherein 2-methyl-6-solanylbenzoquinone methyltransferase is encoded by a nucleic acid sequence comprising
 - i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:1 or in SEQ ID NO:3; or
 - ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO:2 or in SEQ ID NO: 4 by back translation; or
 - iii) a functional equivalent of the nucleic acid sequence SEQ ID NO:3 with at least 59% identity with SEQ ID NO:4.
3. (Previously presented) The method according to claim 2, wherein the amino acid sequence of 2-methyl-6-solanylbenzoquinone methyltransferase is encoded by a nucleic acid sequence comprising
 - i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:1 or in SEQ ID NO:3; or
 - ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO:2 or in SEQ ID NO: 4 by back translation; or
 - iii) a functional equivalent of the nucleic acid sequence SEQ ID NO:3 which can be derived by back translating an amino acid sequence with at least 59% identity with SEQ ID NO:4,

which is truncated by at least 20 amino acids at the C terminus and by at least 20 amino acids at the N terminus.

4. (Previously presented) The method according to claim 3, wherein the amino acid sequence of the truncated 2-methyl-6-solanylbenzoquinone methyltransferase is encoded by a nucleic acid sequence comprising
- i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:5 or in SEQ ID NO:7; or
 - ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO:6 or in SEQ ID NO:8 by back translation.
5. (Previously presented) An isolated nucleic acid sequence encoding a polypeptide with the activity of a 2-methyl-6-solanylbenzoquinone methyltransferase comprising
- i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:5 or in SEQ ID NO:7; or
 - ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO:6 or in SEQ ID NO: 8 by back translation; or
 - iii) SEQ ID NO:1, SEQ ID NO:3 or a functional equivalent of the nucleic acid sequence SEQ ID NO:3 which can be derived by back translating an amino acid sequence with at least 59% identity with SEQ ID NO:4;
- or truncated versions of i), ii), or iii) where the nucleic acid is truncated by at least 20 amino acids at the C terminus and by at least 20 amino acids at the N terminus.
6. (Original) A polypeptide with the activity of a 2-methyl-6-solanylbenzoquinone methyltransferase encoded by a nucleic acid molecule according to claim 5.
7. (Previously presented) An expression cassette comprising genetic control sequences in operable linkage with a nucleic acid sequence according to claim 5 and optionally one or more additional functional elements.

8. (Original) A vector comprising an expression cassette according to claim 7.
9. (Previously presented) A nonhuman transgenic organism comprising at least one nucleic acid sequence according to claim 5, selected from the group consisting of bacteria, yeasts, fungi, animals, and plants.
10. (Original) A method for identifying herbicidally active substances, comprising the following steps:
 - i. bringing a polypeptide with the activity of a 2-methyl-6-solanylbenzoquinone methyltransferase into contact with one or more test compounds under conditions which permit the binding of the test compound(s) to the polypeptide with the activity of a 2-methyl-6-solanylbenzoquinone methyltransferase; and
 - ii. testing whether the test compound binds to the polypeptide with the activity of a 2-methyl-6-solanylbenzoquinone methyltransferase; or
 - iii. detecting whether the test compound reduces or blocks the activity of the polypeptide with the activity of a 2-methyl-6-solanylbenzoquinone methyltransferase of i); or
 - iv. detecting whether the test compound reduces or blocks the transcription, translation or expression of the polypeptide with the activity of a 2-methyl-6-solanylbenzoquinone methyltransferase of i).
11. (Previously presented) The method according to claim 10, wherein the polypeptide with the activity of a 2-methyl-6-solanylbenzoquinone methyltransferase is encoded by a nucleic acid sequence comprising
 - i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:5 or in SEQ ID NO:7; or
 - ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO:6 or in SEQ ID NO: 8 by back translation; or

- iii) SEQ ID NO:1, SEQ ID NO:3 or a functional equivalent of the nucleic acid sequence SEQ ID NO:3 which can be derived by back translating an amino acid sequence with at least 59% identity with SEQ ID NO:4;
or truncated versions of i), ii), or iii) where the nucleic acid sequence is truncated by at least 20 amino acids at the C terminus and by at least 20 amino acids at the N terminus.

12. (Previously presented) The method according to claim 10, wherein the amino acid sequence of 2-methyl-6-solanylbenzoquinone methyltransferase is encoded by a nucleic acid sequence comprising

- i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:1 or in SEQ ID NO:3; or
ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO:2 or in SEQ ID NO: 4 by back translation; or
iii) a functional equivalent of the nucleic acid sequence SEQ ID NO:3 which can be derived by back translating an amino acid sequence with at least 59% identity with SEQ ID NO: 4;

or truncated versions of i), ii), or iii) where the nucleic acid sequence is truncated by at least 20 amino acids at the C terminus and by at least 20 amino acids at the N terminus.

13. (Original) The method according to claim 10, wherein 2-methyl-6-solanylbenzoquinone methyltransferase is encoded by a nucleic acid sequence comprising

- i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:5 or in SEQ ID NO:7; or
ii) a nucleic acid which, owing to the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO:6 or in SEQ ID NO:8 by back translation.

14. (Previously presented) The method according to claim 10, wherein a test compound which reduces or blocks the activity of 2-methyl-6-solanylbenzoquinone methyltransferase is selected.
15. (Previously presented) The method according to claim 14, which comprises
- i. either expressing, in a transgenic organism, a 2-methyl-6-solanylbenzoquinone methyltransferase or culturing an organism which naturally comprises 2-methyl-6-solanylbenzoquinone methyltransferase;
 - ii. bringing the 2-methyl-6-solanylbenzoquinone methyltransferase of step i) in a cell digest of the transgenic or nontransgenic organism, in partially or homogeneously purified form, into contact with a test compound; and
 - iii. selecting a test compound which reduces or blocks the activity of the 2-methyl-6-solanylbenzoquinone methyltransferase of step ii).
16. (Original) The method according to claim 14, which comprises the following steps:
- i. generating a transgenic organism comprising at least one nucleic acid sequence encoding 2-methyl-6-solanylbenzoquinone methyltransferase, in which organism 2-methyl-6-solanylbenzoquinone methyltransferase is overexpressed;
 - ii. applying a test substance to the transgenic organism of i) and to a nontransgenic organism of the same type;
 - iii. determining the growth or the viability of the transgenic and the nontransgenic organisms after application of the test substance; and
 - iv. selecting test substances which bring about a reduced growth or a reduced viability of the nontransgenic organism in comparison with the growth of the transgenic organism.
17. (Previously presented) A method for identifying growth-regulatory substances, which comprises the following steps;

- i. generating a transgenic plant comprising a nucleic acid sequence encoding 2-methyl-6-solanylbenzoquinone methyltransferase, in which plant 2-methyl-6-solanylbenzoquinone methyltransferase is overexpressed;
 - ii. applying a test substance to the transgenic plant of i) and to a nontransgenic plant of the same type;
 - iii. determining the growth or the viability of the transgenic and of the nontransgenic plants after application of the test substance; and
 - iv. selecting test substances which bring about a modified growth of the nontransgenic plant in comparison with the growth of the transgenic plant.
18. (Previously presented) The method according to claim 10, wherein the substances are identified by high-throughput screening.
19. (Previously presented) A support having one or more of the nucleic acid molecules according to claim 5.
20. (Previously presented) The method according to claim 10, wherein the substances are identified by high-throughput screening using a support having one or more nucleic acid molecules comprising an isolated nucleic acid sequence encoding a polypeptide with the activity of a 2-methyl-6-solanylbenzoquinone methyltransferase comprising
- i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:5 or in SEQ ID NO:7; or
 - ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO:6 or in SEQ ID NO: 8 by back translation; or
 - iii) SEQ ID NO:1, SEQ ID NO:3 or a functional equivalent of the nucleic acid sequence SEQ ID NO:3 which can be derived by back translating an amino acid sequence with at least 59% identity with SEQ ID NO:4;
- or truncated versions of i), ii), or iii) where the nucleic acid is truncated by at least 20

amino acids at the C terminus and by at least 20 amino acids at the N terminus.

21. (Previously presented) A herbicidally active compound identified by the method according to claim 10.
22. (Previously presented) A compound with growth-regulatory activity identified via the method according to claim 17.
23. (Previously presented) A process for the preparation of an agrochemical composition, which comprises
- a) identifying a herbicidally active compound according to claim 21; and
 - b) formulating this compound together with suitable auxiliaries to give crop protection compositions with herbicidal or growth-regulatory activity.
24. (Previously presented) A method for controlling undesired vegetation and/or for regulating the growth of plants, which comprises allowing at least one compound according to claim 21 or an agrochemical composition comprising a compound according to claim 21 to act on plants, their environment and/or on seeds.
25. (Previously presented) A method for generating nucleic acid sequences which encode 2-methyl-6-solanylbenzoquinone methyltransferase which are not inhibited by substances according to claim 21, where the nucleic acid sequence comprises
- i) a functional equivalent of the nucleic acid sequence SEQ ID NO:3 which can be derived by back translating an amino acid sequence with at least 59% identity with SEQ ID NO:4; or
 - ii) a functional equivalent of the nucleic acid sequence SEQ ID NO:3 which can be derived by back translating an amino acid sequence with at least 59% identity with SEQ ID NO:4 and which is truncated by at least 20 amino acids at the C terminus and by at least 20 amino acids at the N terminus;

which comprises the following process steps:

- a) expressing, in a heterologous system or in a cell-free system, a protein encoded by the nucleic acid of i) above;
- b) modifying the nucleic acid by randomized or site-directed mutagenesis of the protein;
- c) measuring the interaction of the modified gene product with the herbicide;
- d) identifying derivatives of the protein which exhibit a lesser degree of interaction;
- e) testing the biological activity of the protein after application of the herbicide; and
- f) selecting nucleic acid sequences which exhibit a modified biological activity toward the herbicide.

26. (Previously presented) The method according to claim 25, wherein the selected sequences are introduced into an organism.

27. (Currently amended) A method for generating transgenic plants which are resistant to substances according to claim 20 21, which comprises overexpressing, in a plant, at least one nucleic acid sequence which encodes 2-methyl-6-solanylbenzoquinone methyltransferase, wherein the nucleic acid sequence comprises

- i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:1 or in SEQ ID NO:3; or
- ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO:2 or in SEQ ID NO: 4 by back translation; or
- iii) a functional equivalent of the nucleic acid sequence SEQ ID NO:3 which can be derived by back translating an amino acid sequence with at least 59% identity with SEQ ID NO:4.; or

- iv) a nucleic acid sequence of i), ii) or iii) which is truncated by at least 20 amino acids at the C terminus and by at least 20 amino acids at the N terminus; or
 - v) a nucleic acid with the nucleic acid sequence shown in SEQ ID NO:5 or in SEQ ID NO:7; or
 - vi) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO:6 or in SEQ ID NO:8 by back translation.
28. (Original) A transgenic plant, generated by a method according to claim 27.
29. (Previously presented) A nonhuman transgenic organism comprising an expression cassette according to claim 7, selected from the group consisting of bacteria, yeasts, fungi, animals, and plants.
30. (Previously presented) A nonhuman transgenic organism comprising a vector according to claim 8, selected from the group consisting of bacteria, yeasts, fungi, animals, and plants.
31. (Previously presented) The method according to claim 17, wherein the substances are identified by high-throughput screening.
32. (Previously presented) The method according to claim 17, wherein the substances are identified in a high-throughput screening using a support having one or more nucleic acid molecules comprising a nucleic acid sequence encoding a polypeptide with the activity of a 2-methyl-6-solanylbenzoquinone methyltransferase comprising
- i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO: 5 or in SEQ ID NO: 7; or
 - ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO: 6 or in SEQ ID NO: 8 by back translation; or

- iii) SEQ ID NO: 1, SEQ ID NO: 3 or a functional equivalent of the nucleic acid sequence SEQ ID NO: 3 which can be derived by back translating an amino acid sequence with at least 59% identity with SEQ ID NO: 4; and is truncated by at least 20 amino acids at the C terminus and by at least 20 amino acids at the N terminus.
33. (Previously presented) A process for the preparation of an agrochemical composition, which comprises
- a) identifying a compound with growth-regulatory activity according to claim 22; and
 - b) formulating this compound together with suitable auxiliaries to give crop protection compositions with herbicidal or growth-regulatory activity.
34. (Previously presented) A method for controlling undesired vegetation and/or for regulating the growth of plants, which comprises allowing at least one compound according to claim 22 or an agrochemical composition comprising a compound according to claim 22 to act on plants, their environment and/or on seeds.
35. (Previously presented) The expression cassette of claim 7, wherein the additional functional elements are selected from the group consisting of reporter genes, replication origins, selection markers, affinity tags, and sequences which target products into apoplasts, plastids, vacuoles, mitochondria, peroxisomes, endoplasmatic reticulum (ER), or cytosol.